

60439374, 013007

55 Example 6:

The following example shows a nucleic acid comparison between the gene 2 coding regions from a disease resistant and disease susceptible variety. The top sequence is the gene 2 coding region from the resistant homolog. The bottom sequence is the gene 2 coding region

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from the susceptible 177013 homolog. Note that the susceptible homolog contains a C to G point mutation at position 1362 that creates a stop codon in second exon at Tyr454 (residue 454 of 970 total), creating a severely truncated protein, in addition to one mismatch (C to T) at codon 10 which doesn't change the amino acid and one sense mutation (T to C) at codon 22 which

5 alters valine to alanine.

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1  ATGGCTGAAGCTTTCATTCAACTCTCTCTAGACAACTCTCACTTCCTTCTCT 50
   |||||||
2895 ATGGCTGAAGCTTTCATTCAAGTCTCTGTAGACAACTCTCACTTCCTTCTCT 2846
10 51  CAAGGGBAACTTCTATTCTCTTTTGGCTTTCAAGATGAGCTTCAAGAGG 100
   |||||||
2845 CAAGGGBAACTTGCATTGCTTTTGGCTTTCAAGATGAGTTCCAAAGGC 2796
15 101  TTTCAGAGCATGTTTCTACAAATTCAGAGCCCTCTCTTGAAGATGCTCAGGAG 150
   |||||||
2795 TTTCAGAGCATTTTCTACAAATTCAGAGCCCTCTCTTGAAGATGCTCAGGAG 2746
20 151  AAGCAACTCAACACAGAGCCTCTAGAAATTTGGTGCAAAATCTCAATGC 200
   |||||||
2745 AAGCAACTCAACACAGAGCCTCTAGAAATTTGGTGCAAAATCTCAATGC 2696
25 201  TGCTACATATGAAGTCGATGACATCTTGGATGAATATATAAAACCAAGGCCA 250
   |||||||
2695 TGCTACATATGAAGTCGATGACATCTTGGATGAATATATAAAACCAAGGCCA 2646
30 251  CAAAGATTCTCCAGTCTGAAATATGGCCGTATCATCTCAAGGTATTCCT 300
   |||||||
2645 CAAAGATTCTCCAGTCTGAAATATGGCCGTATCATCTCAAGGTATTCCT 2596
35 301  TTCCGTACAAAGCTCGGGAAGAGATGGACCAAGTGTGAATAAACTAAA 350
   |||||||
2595 TTCCGTACAAAGCTCGGGAAGAGATGGACCAAGTGTGAATAAACTAAA 2546
40 351  GGCATTGTGTGAGGAAAGAAAGATTTTCATTTCACAGCAAAAATTTGTAG 400
   |||||||
2545 GGCATTGTGTGAGGAAAGAAAGATTTTCATTTCACAGCAAAAATTTGTAG 2496
45 401  AGAGNCAAGCTGTATGACGGCAACACGTCCTGTATTAACGAAACCCGAG 450
   |||||||
2495 AGAGNCAAGCTGTATGACGGCAACACGTCCTGTATTAACGAAACCCGAG 2446
50 451  GTTTATGGAAGAGACAAAGACAGATGAGATGAGATGAAATCCATAATA 500
   |||||||
2445 GTTTATGGAAGAGACAAAGACAGATGAGATGAGATGAAATCCATAATA 2396
55 501  CAATGTTAGTGATGCCCAACACCTTTCAGTCTCTCCCAATCTTGGTATGG 550
   |||||||
2395 CAATGTTAGTGATGCCCAACACCTTTCAGTCTCTCCCAATCTTGGTATGG 2346
551  GGGGATTAGGAAAAAGCACTCTTGCCCAAAATGGTCTTCATAGCACAGAG 600
   |||||||
2345 GGGGATTAGGAAAAAGCACTCTTGCCCAAAATGGTCTTCATAGCACAGAG 2296
601  GTTACTGAGCATTTCCATTCCAAATATGGATTTGTGTCTCGGAAGATT 650
   |||||||
2295 GTTACTGAGCATTTCCATTCCAAATATGGATTTGTGTCTCGGAAGATT 2246

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	651	TGAAAGAGAGAGCTTAAATAAGCAACTTGTGAATCATTTGAAGGAGGCG	700
5	2145	TGTGAGGAGAGAGCTTAAATAAGCAACTTGTGAATCATTTGAAGGAGGCG	2196
	701	CACCTACTTGTGAGAGTGACCTTGGTCCACTCAAAAGAGACCTCAGGAG	750
	2195	CACCTACTTGTGAGAGTGACCTTGGTCCACTCAAAAGAGACCTCAGGAG	2146
10	751	TTGCTCAATGCAAAAGATCTTGTCTGTCTAGATGATCTTGCAGATGCA	800
	2145	TTGCTCAATGCAAAAGATCTTGTCTGTCTAGATGATCTTGCAGATGCA	2096
15	801	AGATCAACAAGAGTGGGCTTAATTTAAGACAGCTTTGAAGTGTGCGACAA	850
	2095	AGATCAACAAGAGTGGGCTTAATTTAAGACAGCTTTGAAGTGTGCGACAA	2046
20	851	CTGTCGCTCTTCTTCTAAGCACTACTCTCTTAAAGAGTGGATCAAT	900
	2045	CTGTCGCTCTTCTTCTAAGCACTACTCTCTTAAAGAGTGGATCAAT	1996
	901	ATGGGAGCATCTGCACCATATGAATCTCAAACTGCTTCAAGAGATTTG	950
	1995	ATGGGAGCATCTGCACCATATGAATCTCAAACTGCTTCAAGAGATTTG	1946
25	951	TGTGTTCTTGTCTCATGCAGCTGCTATTGGGACACAGAGAAATAATCT	1000
	1945	TGTGTTCTTGTCTCATGCAGCTGCTATTGGGACACAGAGAAATAATCT	1896
30	1001	CAAACTCTTGCGATCGGAAGAGAGATTTGTGAATAAAGTGTGCTGTG	1050
	1895	CAAACTCTTGCGATCGGAAGAGAGATTTGTGAATAAAGTGTGCTGTG	1796
	1051	CCCTATGACGCAAAACTCTTGGGAGTATTTTGTCTTCAAGAGCAAGA	1100
35	1845	CCCTATGACGCAAAACTCTTGGGAGTATTTTGTCTTCAAGAGCAAGA	1796
	1101	AAGAGCTTGGGAAGTCTTGAGACACAGCTCGATTGGAAATTTGCTCCAG	1150
40	1795	AAGAGCTTGGGAAGTCTTGAGACACAGCTCGATTGGAAATTTGCTCCAG	1746
	1151	ATGAAGTCTCTATTTCGCTGCGCTGAGGCTTAGTATCATCACTTCCA	1200
45	1745	ATGAAGTCTCTATTTCGCTGCGCTGAGGCTTAGTATCATCACTTCCA	1696
	1201	CTTGATTTGAAACATCTCTTGGATATTGTGCGGTGTGCCAAGAGAGCG	1250
	1695	CTTGATTTGAAACATCTCTTGGATATTGTGCGGTGTGCCAAGAGAGCG	1646
50	1251	CAAATTTGAAAAGGAAAGAGCTATCTCTCTTGCTGAGTGCGGCGATTTTC	1300
	1645	CAAATTTGAAAAGGAAAGAGCTATCTCTCTTGCTGAGTGCGGCGATTTTC	1596
55	1301	TTTTATCAAGGAAGCAATGAGCTAGGAGTGTGGGCGATGAAGATGCG	1350
	1595	TTTTATCAAGGAAGCAATGAGCTAGGAGTGTGGGCGATGAAGATGCG	1546
	1351	AAAGTATCAAGTCTTGCGCTCTTTTTCAGAGATGAGTGAAGATGCG	1400
60	1545	AAAGTATCAAGTCTTGCGCTCTTTTTCAGAGATGAGTGAAGATGCG	1496
	1401	TAAACCTATTTCAGATGATGATCTCTCTCCATGATTTGCAACATC	1450

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1495 TAAACTTATTTCAGATGCATGATCTCATCATGATTGGCAACATCTC 1446
1451 TGTTTTCAGCAACACGATCTCAAGCAGCATATCCCTGAATTAATTAACAC 1500
5 1445 TGTTTTCAGCAACACGATCTCAAGCAGCAATATCCCTGAATTAATTAACAC 1396
1501 AGTTACACACATATGATGCCATTTGTTTGGCCGAAGTGGGTTTTTTTA 1550
1395 AGTTACACACATATGATGCCATTTGTTTGGCCGAAGTGGGTTTTTTTA 1346
10 1551 CACTCTTCCGCCCTTGGAAAGTTTATCTGTTTAAGACTGCTTAATCTAG 1600
1345 CACTCTTCCGCCCTTGGAAAGTTTATCTGTTTAAGACTGCTTAATCTAG 1296
15 1601 GTGATTCGCACATTATATAAGTTACCATCTCCATGGAGATCTAGTACAT 1650
1295 GTGATTCGCACATTATATAAGTTACCATCTCCATGGAGATCTAGTACAT 1246
1651 TTAAGATACTTGAACCTGTATGGCAGTGGCATGGCTGACTCTTCCAAAGCA 1700
20 1245 TTAAGATACTTGAACCTGTATGGCAGTGGCATGGCTGACTCTTCCAAAGCA 1196
1701 GTTATGCAGCTTCARAATCTGCNAACTCTTGATCTACAAATTGCAACA 1750
25 1195 GTTATGCAGCTTCARAATCTGCNAACTCTTGATCTACAAATTGCAACA 1146
1751 AGCTTTGTTGTTTCCAAAGCAAGTAAACTTGGTAGTCTCCGAAAT 1800
1145 AGCTTTGTTGTTTCCAAAGCAAGTAAACTTGGTAGTCTCCGAAAT 1096
30 1801 CTTTACTTGATGCTAGCCAGTCTTGTACTTGTATGCCACCAAGGATAGG 1850
1095 CTTTACTTGATGCTAGCCAGTCTTGTACTTGTATGCCACCAAGGATAGG 1046
35 1851 ATCAATGACATGCCCTTAAGACTCTAGGTCAATTTGTTGGAAGGAAG 1900
1045 ATCAATGACATGCCCTTAAGACTCTAGGTCAATTTGTTGGAAGGAAG 996
1901 AAGGTTATCAACTTGGTGAAGTGAAGAACTTAATCTCTATGGCTCAATT 1950
40 995 AAGGTTATCAACTTGGTGAAGTGAAGAACTTAATCTCTATGGCTCAATT 946
1951 AAATCTCGCATCTTGAGAGAGTGAAGAACTGAATGATGGACCAAGGAAGC 2000
45 945 AAATCTCGCATCTTGAGAGAGTGAAGAACTGAATGATGGACCAAGGAAGC 896
2001 CAATTATCTGCAAAAGGGAATCTGCACTTTTAAGCATGAGTTGCAATA 2050
50 895 CAATTATCTGCAAAAGGGAATCTGCACTTTTAAGCATGAGTTGCAATA 846
2051 ACTTTGGACACATATATATGAACTCAGAGAGTGAAGTGGTGGAGGC 2100
845 ACTTTGGACACATATATATGAACTCAGAGAGTGAAGTGGTGGAGGC 796
55 2101 CTCACACCACTCCAACTGACTCTTTAAATCTATGGCTTCAGAGG 2150
795 CTCACACCACTCCAACTGACTCTTTAAATCTATGGCTTCAGAGG 746
2151 ATCCATCTCCAGAGTGGATTAATCACTCAGTATTTGAAATAATGCTCT 2200
60 745 ATCCATCTCCAGAGTGGATTAATCACTCAGTATTTGAAATAATGCTCT 696

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2201 CTATCTCTAATTAGCAACTTCAGAACTGCTCATGCTTACACACCTTTGGT 2250
    |||
695 CTATCTCTAATTAGCAACTTCAGAACTGCTCATGCTTACACACCTTTGGT 646
5
2251 GATCTGCCTTGTCTAGAAAGCTTAGAGTTACACTCGGGGCTTCGGGATGT 2300
    |||
645 GATCTGCCTTGTCTAGAAAGCTTAGAGTTACACTCGGGGCTTCGGGATGT 596
10
2301 GGAGTATCTTTGAGGAAGTGGATATTTGATGTTCTATTCTGGATTCGCCACAA 2350
    |||
595 GGAGTATCTTTGAGGAAGTGGATATTTGATGTTCTATTCTGGATTCGCCACAA 546
15
2351 GAATTAAGTTTTCATCTCTTGGAGAACTTGATATATGGGACTTTGGTAGT 2400
    |||
545 GAATTAAGTTTTCATCTCTTGGAGAACTTGATATATGGGACTTTGGTAGT 496
20
2401 CTGAAGGAGTTCCTCAAAAACGAACTGAGAGAGCAATTCCTGTGCTTGA 2450
    |||
495 CTGAAGGAGTTCCTCAAAAACGAGGAGAGAGCAATTCCTGTGCTTGA 446
25
2451 AGAGATGAGTAATTCAGAGTCCCTTTCTGACCTTTCTCTAACTCTTA 2500
    |||
445 AGAGATGAGTAATTCAGAGTCCCTTTCTGACCTTTCTCTAACTCTTA 396
30
2501 GGGCTCTTACTTCCCTCAGATTTGCTATATTAAGTACTACTTCTCTA 2550
    |||
395 GGGCTCTTACTTCCCTCAGATTTGCTATATTAAGTACTACTTCTCTA 346
35
2551 CCAAGAGAGATGTTCAAAAACCTTGCRAAATCTCAAACTTTGCAATCTC 2600
    |||
345 CCAAGAGAGATGTTCAAAAACCTTGCRAAATCTCAAACTTTGCAATCTC 296
40
2601 TCGGTGCAATTAATCTCAAAGGCTGCTTACCGCTTGGCTAGTCTGAATG 2650
    |||
295 TCGGTGCAATTAATCTCAAAGGCTGCTTACCGCTTGGCTAGTCTGAATG 246
45
2651 CTTTGAAGAGTCTAANAATCAATTTGTTGGGCACTAGAGAGTCTCCCT 2700
    |||
245 CTTTGAAGAGTCTA .....GGCACTAGAGTCTCCCT 214
50
2701 GAGGAGAGGCTGGAGGTTTATCTTCACTCAGCAGATTAATTTGTGAAC 2750
    |||
213 GAGGAGAGGCTGGAGGTTTATCTTCACTCAGCAGATTAATTTGTGAAC 164
55
2751 CTGTACATGCTAANAATGTTTACGAGGGGATTCGACACCTAACAACCC 2800
    |||
163 CTGTACATGCTAANAATGTTTACGAGGGGATTCGACACCTAACAACCC 114
60
2801 TCAAGAGTTTAAANAATTCGGGATGTCACAACCTGATCAGCGGTGTGAG 2850
    |||
113 TCAAGAGTTTAAANAATTCGGGATGTCACAACCTGATCAGCGGTGTGAG 64
2851 AAGGGAGATGGAGAGACTGGCACAANAATCTCACATTCCTAATGTGAA 2900
    |||
63 AAGGGAGATGGAGAGACTGGCACAANAATCTCACATTCCTAATGTGAA 14
2901 TATATATATTTAA 2913
    |||
13 TATATATATTTAA 1

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